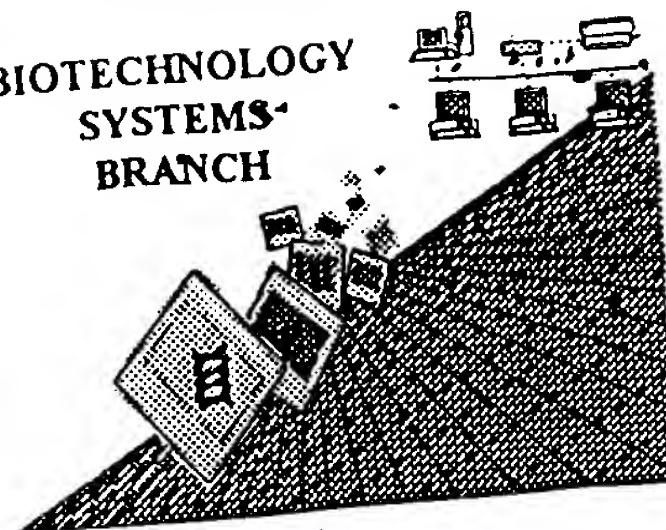


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



W 10
1026

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/974870

Source: OIPE

Date Processed by STIC: 10/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/974870

ERROR DETECTED

SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P1

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length.

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ☒ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/974,870

DATE: 10/30/2001
TIME: 12:00:55

Input Set : A:\pto_vsk.txt
Output Set: N:\CRF3\10302001\I974870.raw

3 <110> APPLICANT: Whitcombe, David M
4 Theaker, Jane
5 Gibson, Neil J
6 Little, Stephen
8 <120> TITLE OF INVENTION: Methods for Detecting Nucleic Acid Sequences
10 <130> FILE REFERENCE: 1991-143
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/974,870
C--> 13 <141> CURRENT FILING DATE: 2001-10-12
15 <150> PRIOR APPLICATION NUMBER: UK/9812768.1
16 <151> PRIOR FILING DATE: 1998-06-13
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 60
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: B2098-BRCA
29 Scorpions primer
31 <220> FEATURE:
32 <221> NAME/KEY: stem_loop
33 <222> LOCATION: (1)..(29)
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (30)
38 <223> OTHER INFORMATION: n = MR = a non-fluorogenic fluorophore attached to
39 a uracil
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (31)
44 <223> OTHER INFORMATION: n = HEG = blocking hexethylene glycol monomer
46 <400> SEQUENCE: 1
W--> 47 cgcacgatgt agcacatcag aagcgtgcn nttggagatt ttgtcacttc cactctcaaa 60
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 29
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence: R186-98,
57 Untailed equivalent of B2098 primer
59 <400> SEQUENCE: 2
60 ttggagattt tgtcacttcc actctcaaa 29
63 <210> SEQ ID NO: 3
64 <211> LENGTH: 30
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:

Does Not Comply
Corrected Diskette Needed

*use of n
n must represent
nucleotide values
nms*

*The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/974,870

DATE: 10/30/2001
 TIME: 12:00:55

Input Set : A:\pto_vsk.txt
 Output Set: N:\CRF3\10302001\I974870.raw

69 <223> OTHER INFORMATION: Description of Artificial Sequence: Z3702, Probe
 70 segment of the Scorpions B2098 primer
 72 <220> FEATURE:
 73 <221> NAME/KEY: stem_loop
 74 <222> LOCATION: (1)..(29)
 76 <220> FEATURE:
 77 <221> NAME/KEY: misc_feature
 78 <222> LOCATION: (30)
 79 <223> OTHER INFORMATION: n = MR = a non-fluorogenic fluorophore attached to
 80 a uracil
 82 <400> SEQUENCE: 3
 W--> 83 cgcacgatgt agcacatcag aagcgtgcgn 30
 86 <210> SEQ ID NO: 4
 87 <211> LENGTH: 50
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Artificial Sequence
 91 <220> FEATURE:
 92 <223> OTHER INFORMATION: Description of Artificial Sequence: B2731 Scorpion
 93 primer
 95 <220> FEATURE:
 96 <221> NAME/KEY: misc_feature
 97 <222> LOCATION: (18)
 98 <223> OTHER INFORMATION: n = MR = a non-fluorogenic fluorophore attached to
 99 a uracil
 101 <220> FEATURE:
 102 <221> NAME/KEY: misc_feature
 103 <222> LOCATION: (19)
 104 <223> OTHER INFORMATION: n = H = blocking hexethylene glycol monomer
 106 <400> SEQUENCE: 4
 W--> 107 aggtagtgcga gagagtgnng agcctcaaca tcctgctccc ctctactac 50
 110 <210> SEQ ID NO: 5
 111 <211> LENGTH: 49
 112 <212> TYPE: DNA
 113 <213> ORGANISM: Artificial Sequence
 115 <220> FEATURE:
 116 <223> OTHER INFORMATION: Description of Artificial Sequence: B4249 Scorpion
 117 primer without quencher on same molecule
 119 <220> FEATURE:
 120 <221> NAME/KEY: misc_feature
 121 <222> LOCATION: (18)
 122 <223> OTHER INFORMATION: n = h = blocking hexethylene glycol monomer
 124 <400> SEQUENCE: 5
 W--> 125 aggtagtgcga gagagtgnnga gcctcaacat cctgctcccc tcctactac 49
 128 <210> SEQ ID NO: 6
 129 <211> LENGTH: 18
 130 <212> TYPE: DNA
 131 <213> ORGANISM: Artificial Sequence
 133 <220> FEATURE:
 134 <223> OTHER INFORMATION: Description of Artificial Sequence: Quencher

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/974,870

DATE: 10/30/2001

TIME: 12:00:55

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF3\10302001\I974870.raw

```

135      oligonucleotide for B4249 (complement tail)
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: (18)
140 <223> OTHER INFORMATION: n = MR = a non-fluorogenic fluorophore attached to
141      a uracil
143 <400> SEQUENCE: 6
W--> 144 cactctctgc actacctn                                18
147 <210> SEQ ID NO: 7
148 <211> LENGTH: 28
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: ARMS primer
154      R284-97
156 <400> SEQUENCE: 7
157 ttcggggctc cacacggcga ctctcaac                                28
160 <210> SEQ ID NO: 8
161 <211> LENGTH: 28
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Description of Artificial Sequence: ARMS primer
167      R283-97
169 <400> SEQUENCE: 8
170 ttcggggctc cacacggcga ctctcaag                                28

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/974,870

DATE: 10/30/2001

TIME: 12:00:56

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF3\10302001\I974870.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6